REMARKS

Claims 1-14 have been withdrawn as being drawn to a non-elected restriction group. Claims 26 and 28 have been amended, and new claims 31 and 32 have been added. Support for the new and amended claims can be found throughout the specification as filed, e.g., at page 7, lines 9-12; page 10, lines 18-20; and original claims 26, 28, 29 and 30. No new matter has been added.

Upon entry of the amendments above, claims 15-32 will be pending.

Telephonic Communication With Examiner

Applicant thanks Examiner Parkin for taking the time on July 27, 2004, to conduct a telephonic conference with Applicant's representative. During the conference, Applicant's representative requested clarification of the present rejections under 35 U.S.C. § 102(b). Applicant's representative requested guidance as to which sequences were being cited as allegedly anticipating in the Office Action paper of July 24, 2004. Applicant's representative explained that such guidance was needed, especially with respect to the cited reference WO 96/40933, which includes over 200 pages of text and drawings and discloses 173 different sequences. Examiner Parkin indicated that he would order a new copy of the sequence search results, and would subsequently provide Applicant with the requested guidance. To clarify the record, Applicant's representative did not receive the requested guidance telephonically.

Applicant thanks the Examiner for providing the requested guidance in the Interview Summary form PTOL-413, mailed August 24, 2004.

Legible Replacement Copies of Papers

The Office Action requires replacement copies of the Information Disclosure Statement and Sequence Listing papers that were submitted on February 28, 2002 and June 13, 2002, respectively. Applicant submits herewith a new Information Disclosure Statement, PTO form-1449, and references cited therein. The form PTO-1449 includes all references listed on the previously filed form PTO-1449, and also includes the additional reference (Desig ID. **AO**).

Submitted herewith is a paper copy of the Sequence Listing that is **identical** to the copy previously filed on June 13, 2002, therefore, Applicant declares under 37 C.F.R. 1.821(f) that the content of the paper copy of the Sequence Listing is the same as the machine-readable copy of the Sequence Listing submitted on June 13, 2002, in agreement with the previously submitted verified statement under 37 C.F.R. 1.821(f) also filed June 13, 2002. No new matter has been added.

Rejections

Rejections Under 35 U.S.C. §102(b) Anticipation

WO 96/40933 (Bhamarapravati et al.)

Claims 23-28 stand rejected under 35 U.S.C. §102(b) as allegedly anticipated by WO 96/40933 (Bhamarapravati et al.). Form PTOL-413 mailed August 24, 2004, clarifies that the allegedly anticipating sequences are the sequences referred to as "D2-134", and "D2-274" on page 100 of Bhamarapravati et al.[1] Applicant traverses this rejection as to original claims 23-25, 27, and 28 and amended claim 26.[2]

1. Claims 23-25

Claims 23-25 recite nucleic acids of differing lengths between 18-28 nucleotides in length that include at least 18 consecutive nucleotides of SEQ ID NO:1. Sequence D2-134 (134) and sequence D2-274 (274) each fail to anticipate claims 23-25, because neither sequence has 18 consecutive nucleotides from SEQ ID NO:1. The 134 sequence is not even similar to SEQ ID NO:1. Although the 274 sequence does contain 18 consecutive nucleotides that are reverse-complementary to 18 nucleotides in SEQ ID NO:1, it does not include 18 consecutive nucleotides of SEQ ID NO:1. Furthermore, the 274 sequence is 32 nucleotides in length, and

[1] Although not stated in the form PTOL-413, mailed August 24, 2004, it is apparent that the D2-134 sequence is being cited as anticipating claims that recite of SEQ ID NO:1, and the D2-274 sequence is being cited as anticipating claims directed to SEQ ID NO:2.

[2] The nucleic acids recited by claims 23-28 are useful as reagents in methods that specifically detect all four known Dengue-virus serotypes (Den-1, Den-2, Den-3, and Den-4) and do not detect other flaviviruses.

thus, the 274 sequence is outside the scope of claims 23-25 (which recite nucleic acids that are 18-28 nucleotides in length).

Applicants also point out that the 274 sequence does not render the nucleic acids of claims 23-25 obvious. Bhamarapravati et al. provides no suggestion to use the currently claimed nucleic acids, which are reverse-complementary to the 274 sequence. Applicants also submit that modifying the 274 sequence by making the sequence a reverse-complementary sequence fragment of the disclosed 274 sequence, would render the sequence unsuitable for its intended use in Bhamarapravati et al. Without changing other parameters in the reaction, a primer cannot simply be substituted with a reverse-complementary primer in any of the following reactions: RT-PCR, PCR, or nucleotide sequencing. Such a substitution either changes the product of the reaction or renders the reaction non-functional. The currently claimed nucleic acids are therefore not rendered obvious by the 274 sequence, absent any suggestion to use reverse-complementary sequences of 274.

2. Claims 26-28

Claim 26, as amended, and original claim 27 recite nucleic acid molecules of differing lengths, between 18-25 nucleotides in length, that include at least 18 consecutive nucleotides of SEQ ID NO:2. Since the 274 and 134 sequences are 32 and 28 nucleotides in length, respectively, these two sequences are outside the scope of amended claim 26 and claim 27.

Claim 28 has been amended to be in independent claim format. Claim 28 recites a nucleic acid that is the sequence of SEQ ID NO:2. Neither the 274 nor the 134 sequence is SEQ ID NO:2. The 274 sequence is not even similar to SEQ ID NO:2. The 134 sequence includes two nucleotides at its 5' end that are not included in SEQ ID NO:2, and it is missing two nucleotides at the 3' end of SEQ ID NO:2. Therefore, claim 28 does not read on either of the Bhamarapravati et al. sequences cited by the Examiner.

The 134 and 274 sequences disclosed in Bhamarapravati et al. do not teach every element recited by the presently amended claims. For the reasons presented above, Applicant respectfully requests that this rejection be withdrawn as to the presently amended claims.

Kawano et al., *J. Virol.*, 67:6567-6575, 1993

Claims 29 and 30 stand rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Kawano et al., *J. Virol.*, 67:6567-6575, 1993 (Kawano et al.). The Office Action states that (i) Kawano et al. discloses nucleic acid fragments obtained from one of the structural genes of Dengue virus type-4, and (ii) that the fragments encompass SEQ ID NO:1 and SEQ ID NO:2. Applicant traverses this rejection as to all claims.

Claims 29 and 30 recite a fragment of a dengue viral genome, or a DNA copy thereof, with the following elements: (i) a region flanked by SEQ ID NO:1 (first sequence) and SEQ ID NO:2 (second sequence) and (ii) "a non-naturally occurring deletion or insertion" located within the region of the fragment flanked by the first and the second sequence.[3] The fragments disclosed in Kawano et al. do not contain a non-naturally occurring deletion or insertion between the first and second sequence recited by claims 29 and 30. Since Kawano et al. does not teach every element recited by claims 29 and 30, this reference does not anticipate the rejected claims.

For the reasons presented above, Applicant respectfully requests that this rejection be withdrawn.

Unspecified Rejections

The Office Action Summary indicates under the Disposition of the Claims that claims 15-30 are rejected. However, the Detailed Office Action provides no basis for the rejection of claims 15-22. Because the Examiner has the burden of providing the statutory basis for a rejection, and no such basis has been provided, Applicant respectfully requests that the unsupported rejection of claims 15-22 be withdrawn.

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[3] The nucleic acids recited by claims 29 and 30 are useful as competitor RNA (and/or templates for generating competitor RNA), which can be used in the disclosed quantitative Dengue virus detection assays. See, e.g., Example 2 in the specification. These quantitative assays compare the amplified product from target Dengue viral RNA in a sample to the amplified product from known amounts of competitor RNA. To compare the two products, the two products must be readily distinguishable, e.g., by gel electrophoresis. The absence of a non-naturally occurring deletion or insertion in the Kawano et al. fragments prevents these fragments from being useful as a source of competitor RNA. In the disclosed assays, the Kawano et al. fragments would produce an amplified product that is the same length as the amplified product from target Dengue viral RNA, and thus, these two products could not be readily distinguished, e.g., by gel electrophoresis. In fact, in the case of a sample from a subject with a DEN-4 Dengue virus infection, the amplified product generated by the Kawano et al. fragments would be identical to (and therefore impossible to distinguish from) the amplified target Dengue viral product.

Applicant respectfully requests entry of the amendments above and withdrawal of the present rejections. Applicant also requests (i) entry of the paper copy of the Sequence Listing filed herewith and (ii) consideration of the references referred to in the enclosed Information Disclosure Statement.

Please apply any charges or credits to deposit account 06-1050, referencing Attorney No. 12563-004001.

Respectfully submitted,

Date: 9-24-04

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